IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

REQUEST FOR FILING NATIONAL PHASE OF
PCT APPLICATION UNDER 35 U.S.C. 371 AND 37 CFR 1.494 OR 1.495

To: Hon. Commissioner of Patents
Washington, D.C. 20231

00909

TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US)

Atty Dkt: P 277177 /Z 70390/UST
M# /Client Ref.

From: Pillsbury Winthrop LLP, IP Group:

Date: March 16, 2001

This is a **REQUEST** for **FILING** a PCT/USA National Phase Application based on:

1. International Application	2. International Filing Date	3. Earliest Priority Date Claimed
PCT/GB99/03071	15 September 1999	19 September 1998
⇧ country code	Day MONTH Year	Day MONTH Year
		(use item 2 if no earlier priority)

4. Measured from the earliest priority date in item 3, this PCT/USA National Phase Application Request is being filed within:

(a) ☐ 20 months from above item 3 date (b) ☒ 30 months from above item 3 date,

(c) Therefore, the due date (unextendable) is March 19, 2001

5. Title of Invention POLYMORPHISMS IN THE HUMAN ALPHA4 INTEGRIN SUBUNIT GENE, SUITABLE FOR DIAGNOSIS AND TREATMENT OF INTEGRIN LIGAND MEDIATED DISEASES

6. Inventor(s) MORTEN, John Edward Norris

Applicant herewith submits the following under 35 U.S.C. 371 to effect filing:

7. ☒ Please immediately start national examination procedures (35 U.S.C. 371 (f)).

8. ☒ **A copy of the International Application** as filed (35 U.S.C. 371(c)(2)) is transmitted herewith (file if in English but, if in foreign language, file only if not transmitted to PTO by the International Bureau) including:

a. ☒ Request;
b. ☒ Abstract;
c. 29 pgs. Spec. and Claims;
d. _____ sheet(s) Drawing which are ☐ informal ☐ formal of size ☐ A4 ☐ 11"

9. ☒ **A copy of the International Application has been transmitted by the International Bureau.**

10. **A translation of the International Application** into English (35 U.S.C. 371(c)(2))
a. ☐ is transmitted herewith including: (1) ☐ Request; (2) ☐ Abstract;
(3) _____ pgs. Spec. and Claims;
(4) _____ sheet(s) Drawing which are:
☐ informal ☐ formal of size ☐ A4 ☐ 11"
b. ☐ is not required, as the application was filed in English.
c. ☐ is not herewith, but will be filed when required by the forthcoming PTO Missing Requirements Notice per Rule 494(c) if box 4(a) is X'd or Rule 495(c) if box 4(b) is X'd.
d. ☐ Translation verification attached (not required now).

11. ☒ **PLEASE AMEND** the specification before its first line by inserting as a separate paragraph:
a. ☒ --This application is the national phase of international application PCT/GB99/03071 filed September 15, 1999 which designated the U.S.--
b. ☐ --This application also claims the benefit of U.S. Provisional Application No. 60/_____, filed _____ .--

12. ☐ Amendments to the claims of the International Application **under PCT Article 19 (35 U.S.C. 371(c)(3)), i.e., before 18th month from first priority date above in item 3, are transmitted herewith (file only if in English) including:**

13. ☒ PCT Article 19 claim amendments (if any) have been transmitted by the International Bureau

14. ☐ Translation of the amendments to the claims **under PCT Article 19 (35 U.S.C. 371(c)(3)), i.e., of claim amendments** made before 18th month, **is attached (required by 20th month from the date in item 3 if box 4(a) above is X'd, or 30th month if box 4(b) is X'd, or else amendments will be considered canceled).**

15. **A declaration of the inventor** (35 U.S.C. 371(c)(4)).
a. ☒ is submitted herewith ☒ Original ☐ Facsimile/Copy
b. ☐ is not herewith, but will be filed when required by the forthcoming PTO Missing Requirements Notice per Rule 494(c) if box 4(a) is X'd or Rule 495(c) if box 4(b) is X'd.

16. **An International Search Report (ISR):**
a. Was prepared by ☒ European Patent Office ☐ Japanese Patent Office ☐ Other
b. ☒ has been transmitted by the international Bureau to PTO.
c. ☒ copy herewith (3 pg(s).) ☒ plus Annex of family members (1 pg(s).).

17. **International Preliminary Examination Report** (IPER):
a. ☒ has been transmitted (if this letter is filed after 28 months from date in item 3) in English by the International Bureau with Annexes (if any) in original language.
b. ☒ copy herewith in English.
c.1 ☐ IPER Annex(es) in original language ("Annexes" are amendments made to claims/spec/drawings during Examination) including attached amended:
c.2 ☐ Specification/claim pages #_____ claims # Dwg Sheets #
d. ☐ Translation of Annex(es) to IPER **(required by 30th month due date, or else annexed amendments will be considered canceled).**

18. **Information Disclosure Statement** including:
a. ☒ Attached Form PTO-1449 listing documents
b. ☐ Attached copies of documents listed on Form PTO-1449
c. ☒ A concise explanation of relevance of ISR references is given in the ISR.

19. ☒ **Assignment** document and Cover Sheet for recording are attached. Please mail the recorded assignment document back to the person whose signature, name and address appear at the end of this letter.

20. ☐ Copy of Power to IA agent.

21. ☐ **Drawings** (complete only if 8d or 10a(4) not completed): ___ sheet(s) per set: ☐ 1 set informal; ☐ Formal of size ☐ A4 ☐ 11"

22. Small Entity Status ∅ ☒ is **Not** claimed ☐ is claimed (**pre**-filing confirmation required)
22(a) _____ (No.) Small Entity Statement(s) enclosed (since 9/8/00 Small Entity Statements(s) not essential to make claim)

23. **Priority** is hereby claimed under 35 U.S.C. 119/365 based on the priority claim and the certified copy, both filed in the International Application during the international stage based on the filing in (country) GREAT BRITAIN of:

	Application No.	Filing Date		Application No.	Filing Date
(1)	9820339.1	Sept. 19, 1998	(2)	9824506.1	Nov. 10, 1998
(3)			(4)		
(5)			(6)		

a. ☒ See Form PCT/IB/304 sent to US/DO with copy of priority documents. If copy has not been received, please proceed promptly to obtain same from the IB.
b. ☐ Copy of Form PCT/IB/304 attached.

RE: USA National Filing of PCT/GB99/03071

24. Attached: 3 pages of Sequence Listing and 2 copies of form PCT/IB/306

25. **Preliminary Amendment:**

25.5 Per Item 17.c2, **cancel original** pages #_____, claims #_____, Drawing Sheets #

26. **Calculation of the U.S. National Fee (35 U.S.C. 371 (c)(1)) and other fees is as follows:**
Based on amended claim(s) per above item(s) ☐ 12, ☐ 14, ☐ 17, ☐ 25, ☐ 25.5 (hilite)

Total Effective Claims	13	minus 20 =	0	x $18/$9 =	$0	966/967
Independent Claims	7	minus 3 =	4	x $80/$40 =	$320	964/965
If any proper (ignore improper) Multiple Dependent claim is present,				add$270/$135	+270	968/969

BASIC NATIONAL FEE (37 CFR 1.492(a)(1)-(4)): →→ **BASIC FEE REQUIRED, NOW** →→→→

A. If country code letters in item 1 are **not** "US","BR","BB","TT","MX","IL" "NZ", "IN" or "ZA"

See item 16 re:

1.	Search Report was not prepared by EPO or JPO - - - - - - - - -	add$1000/$500	960/961
2.	Search Report was prepared by EPO or JPO - - - - - - - - - - -	add$860/$430 +860	970/971

SKIP B, C, D AND E UNLESS country code letters in item 1 are "US","BR","BB","TT","MX","IL", "NZ", "IN" or "ZA"

→ ☐ B.	If USPTO did not issue both International Search Report (ISR) and (if box 4(b) above is X'd) the International Examination Report (IPER), - - - - - - - - - - - - - - - - - - -	add$970/$485 +0	960/961
☐ C.	If USPTO issued ISR but not IPER (or box 4(a) above is X'd), -	add$710/$355 +0	958/959
→ ☐ D.	If USPTO issued IPER but IPER Sec. V boxes not all 3 YES, -	add$690/$345 +0	956/957
→ ☐ E.	If international preliminary examination fee was paid to USPTO and Rules 492(a)(4) and 496(b) satisfied (IPER Sec. V all 3 boxes YES for all claims), - - - - - - - - - - - - -	add $100/$50 +0	962/963

27. **SUBTOTAL =** $1450

28. If Assignment box 19 above is X'd, add Assignment Recording fee of ----$40 +40 (581)

29. Attached is a check to cover the - **TOTAL FEES** $1490

Our Deposit Account No. 03-3975
Our Order No. 9901 (C#) 277177 (M#)

00909

CHARGE STATEMENT: The Commissioner is hereby authorized to charge any fee specifically authorized hereafter, or any missing or insufficient fee(s) filed, or asserted to be filed, or which should have been filed herewith or concerning any paper filed hereafter, and which may be required under Rules 16-18 and 492 (missing or insufficient fee only) now or hereafter relative to this application and the resulting Official document under Rule 20, or credit any overpayment, to our Account/Order Nos. shown above for which purpose a duplicate copy of this sheet is attached.
This CHARGE STATEMENT does not authorize charge of the issue fee until/unless an issue fee transmittal form is filed

Pillsbury Winthrop LLP
Intellectual Property Group

By Atty: Donald J. Bird **Reg. No.** 25323

Sig:

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Atty/Sec: DJB/mhn

NOTE: File in duplicate with 2 postcard receipts (PAT-103) & attachments.

POLYMORPHISMS IN THE HUMAN ALPHA4 INTEGRIN SUBUNIT GENE, SUITABLE FOR DIAGNOSIS AND TREATMENT OF INTEGRIN LIGAND MEDIATED DISEASES

This invention relates to polymorphisms in the human α_4 integrin subunit gene. The invention also relates to methods and materials for analysing allelic variation in the α_4 integrin subunit gene, and to the use of α_4 integrin subunit polymorphism in the diagnosis and treatment of integrin ligand mediated diseases such as multiple sclerosis, rheumatoid arthritis, atherosclerosis and allergic asthma.

The integrins are a family of heterodimeric cell surface receptors that are composed of noncovalently associated glycoprotein subunits (α and β) and are involved in the adhesion of cells to other cells or to extracellular matrix. The interactions between integrins and their protein ligands are fundamental for maintaining cell function, for example by tethering cells at a particular location, facilitating cell migration, or providing survival signals to cells from their environment. Ligands recognised by integrins include extracellular matrix proteins, such as collagen and fibronectin; plasma proteins, such as fibrinogen; and cell surface molecules, such as transmembrane proteins of the immunoglobulin superfamily and cell-bound complement. There are at least 14 different human integrin α subunits and at least 8 different β subunits and each β subunit can form a heterodimer with one or more α subunits. The specificity of the interaction between integrin and ligand is governed by the α and β subunit composition.

The α_4 integrin subunit comprises 999 amino acids and is formed from a 1038 amino acid precursor by the cleavage of a 39 amino acid N-terminal signal peptide. The core protein molecular weight is 111 kDa. There are 11 N-glycosylation sites in the extracellular region and the protein expressed on the cell surface usually has a molecular weight of 145 kDa, although it can also exist as a 180 kDa isoform. The 145 kDa form can be partially cleaved into 80 and 70 kDa fragments. The extracellular domain comprises amino acid residues 1-944, the transmembrane domain residues 945-967 and there is a short intracellular domain comprising residues 968-999. The N-terminal 432 amino acids contain seven sequence repeats which are thought to fold into a seven-bladed β-propeller. Ligands and a putative magnesium ion are predicted to bind to the upper face of the β-propeller while there are three calcium binding motifs on the lower face.

The α_4 subunit is known to form a heterodimer with either the β_1 or β_7 subunits. The integrin $\alpha_4\beta_1$, also known as Very Late Antigen-4 (VLA-4) or CD49d/CD29, is expressed on numerous hematopoietic cells, including hematopoietic precursors, peripheral and cytotoxic T

lymphocytes, B lymphocytes, monocytes, thymocytes and eosinophils, and established cell lines. $\alpha_4\beta_1$ has two main ligands, Vascular Cell Adhesion Molecule-1 (VCAM-1), also known as CD106, an immunoglobulin superfamily member expressed on the surface of activated vascular endothelial cells and a variety of other cells including dendritic cells, macrophages and fibroblasts, and an isoform of fibronectin containing the alternatively spliced type III connecting segment (CS-1 fibronectin). $\alpha_4\beta_7$ also recognises VCAM-1 and CS-1 fibronectin as ligands but will preferentially bind to Mucosal Addressin Cell Adhesion Molecule-1 (MAdCAM-1), another immunoglobulin superfamily member expressed on vascular endothelial cells, mainly in the small intestine and to a lesser extent the colon and spleen. $\alpha_4\beta_7$ is expressed on lymphocytes that preferentially home to gastrointestinal mucosa and gut-associated lymphoid tissue and may have a role in maintaining mucosal immunity.

The activation and extravasation of blood leukocytes plays a major role in the development and progression of inflammatory diseases. Cell adhesion to the vascular endothelium is required before cells migrate from the blood into inflamed tissue and is mediated by specific interactions between cell adhesion molecules on the surface of vascular endothelial cells and circulating leukocytes. α_4 integrins are believed to have an important role in the recruitment of lymphocytes, monocytes and eosinophils during inflammation.

The affinity of leukocyte integrins for their ligands is normally low but activation of leukocytes increases integrin affinity. At sites of inflammation, leukocyte integrins are thought to be activated by chemokines which act via receptors on the leukocyte surface. Integrin affinity is thought to be regulated by conformational changes in the integrin subunits induced by intracellular signalling pathways acting on the integrin cytoplasmic tails.

Expression of α_4 integrin ligands is upregulated at sites of inflammation. VCAM-1 and MAdCAM-1 expression is upregulated on endothelial cells in vitro by inflammatory cytokines. VCAM-1 expression is upregulated in human inflammatory diseases such as rheumatoid arthritis, multiple sclerosis, allergic asthma and atherosclerosis while CS-1 fibronectin expression is upregulated in rheumatoid arthritis. MAdCAM-1 expression is upregulated in murine models of inflammatory bowel disease and insulin-dependent diabetes.

Monoclonal antibodies directed against the α_4 integrin subunit have been shown to be effective in a number of animal models of human inflammatory diseases including multiple sclerosis, rheumatoid arthritis, allergic asthma, contact dermatitis, transplant rejection, insulin-dependent diabetes, inflammatory bowel disease, and glomerulonephritis.

$\alpha_4\beta_1$ /ligand binding has also been implicated in T-cell proliferation, B-cell localisation to germinal centres, haematopoietic progenitor cell localisation in the bone marrow, angiogenesis, placental development, muscle development and tumour cell metastasis.

Integrins recognise short peptide motifs in their ligands. The minimal α_4 integrin binding epitope in CS-1 is the tripeptide leucine-aspartic acid-valine (LDV) while VCAM-1 contains the similar sequence isoleucine-aspartic acid-serine (IDS). $\alpha_4\beta_7$ binds to a leucine-aspartic acid-threonine (LDT) motif in MAdCAM-1. Small molecule inhibitors of ligand binding to α_4 integrins have been designed based on these short peptide motifs. α_4 integrin antagonists, monoclonal antibodies directed at $\alpha 4$ integrins or their ligands and inhibitors of α_4 integrin ligand expression may have utility in the treatment of autoimmune, allergic and vascular inflammatory diseases, the prevention of tumour metastasis and in mobilisation of haematopoietic progenitor cells from bone marrow prior to tumour chemotherapy.

A cDNA encoding the α_4 integrin subunit has been cloned and published as a EMBL Accession number: L12002 (3567 bp). Promoter sequence has been published as EMBL Accession numbers L26059 and M62841. All positions herein relate to the position therein unless stated otherwise or apparent from the context.

Szabo and McIntyre (1995), Molecular Immunology 32, 1543-54, disclosed a SNP in human integrin α_4 subunit at position 3061, which produces a Gln to Arg change in the subunit.

One approach is to use knowledge of polymorphisms to help identify patients most suited to therapy with particular pharmaceutical agents (this is often termed "pharmacogenetics") . Pharmacogenetics can also be used in pharmaceutical research to assist the drug selection process. Polymorphisms are used in mapping the human genome and to elucidate the genetic component of diseases. The reader is directed to the following references for background details on pharmacogenetics and other uses of polymorphism detection: Linder *et al.* (1997), Clinical Chemistry, **43**, 254; Marshall (1997), Nature Biotechnology, **15**, 1249; International Patent Application WO 97/40462, Spectra Biomedical; and Schafer *et al.* (1998), Nature Biotechnology, **16**, 33.

Clinical trials have shown that patient response to treatment with pharmaceuticals is often heterogeneous. Thus there is a need for improved approaches to pharmaceutical agent design and therapy.

Variations in polypeptide sequence will be referred to as follows: original amino acid (using 1 or 3 letter nomenclature) , position, new amino acid. For (a hypothetical) example "D25K" or "Asp25Lys" means that at position 25 an aspartic acid (D) has been changed to lysine (K). Multiple mutations in one polypeptide will be shown between square brackets with individual mutations separated by commas.

The present invention is based on the discovery of five single nucleotide polymorphisms (SNPs) in the coding region of the human α_4 integrin subunit gene and eight in the promoter region.

According to one aspect of the present invention there is provided a method for the diagnosis of a single nucleotide polymorphism in a α_4 integrin subunit in a human, which method comprises determining the sequence of the nucleic acid of the human at one or more of the following positions:

positions 740, 2273, 2446, 3311 and 3506 in the coding region of α_4 integrin subunit gene as defined by the positions in EMBL ACCESSION NO. L12002;

position 967 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. L26509; and

positions 184, 238, 331, 436, 676, 1010, or 1115 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. M26841;

and determining the status of the human by reference to polymorphism in the α_4 integrin subunit gene.

According to another aspect of the present invention there is provided a method for the diagnosis of a single nucleotide polymorphism in a α_4 integrin subunit in a human, which method comprises determining the sequence of the nucleic acid of the human at one or more of positions 740, 2273, 2446, 3311 and 3506 in the α_4 integrin subunit gene as defined by the positions in EMBL ACCESSION NO. L12002, and determining the status of the human by reference to polymorphism in the α_4 integrin subunit gene.

The term human includes both a human having or suspected of having a α_4 integrin subunit ligand mediated disease and an asymptomatic human who may be tested for predisposition or susceptibility to such disease. At each position the human may be homozygous for an allele or the human may be a heterozygote.

The polymorphisms identified in the present invention which occur in the promoter region are not expected to alter any amino acid sequence, but several of the polymorphisms

affect transcription sites within the promoter region and thus may affect the transcription of the gene. The reader is referred to Example 3 below.

Assays, for example reporter-based assays, may be devised to detect whether one or more of the above polymorphisms affect transcription levels and/or message stability.

Individuals who carry particular allelic variants of the gene may therefore exhibit differences in their ability to regulate protein biosynthesis under different physiological conditions and will display altered abilities to react to different diseases. In addition, differences in protein regulation arising as a result of allelic variation may have a direct effect on the response of an individual to drug therapy. The diagnostic methods of the invention may be useful both to predict the clinical response to such agents and to determine therapeutic dose.

In one embodiment of the invention preferably the method for diagnosis described herein is one in which the single nucleotide polymorphism at position 740 is presence of C and/or T.

In another embodiment of the invention preferably the method for diagnosis described herein is one in which the single nucleotide polymorphism at position 2273 is presence of A and/or G.

In another embodiment of the invention preferably the method for diagnosis described herein is one in which the single nucleotide polymorphism at position 2446 is presence of C and/or T. Testing for the presence of the T allele at this position is especially preferred because, without wishing to be bound by theoretical considerations, of its association with a significant amino acid change in the polypeptide sequence of α_4 integrin.

In another embodiment of the invention preferably the method for diagnosis described herein is one in which the single nucleotide polymorphism at position 3311 is presence of T and/or C.

In another embodiment of the invention preferably the method for diagnosis described herein is one in which the single nucleotide polymorphism at position 3506 is presence of C and/or T.

In another embodiment of the invention preferably the method for diagnosis described herein is one in which the single nucleotide polymorphism at position 967 is presence of G and/or A.

In another embodiment of the invention preferably the method for diagnosis described herein is one in which the single nucleotide polymorphism at position 184 is presence of A and/or G.

In another embodiment of the invention preferably the method for diagnosis described herein is one in which the single nucleotide polymorphism at position 238 is presence of C and/or T.

In another embodiment of the invention preferably the method for diagnosis described herein is one in which the single nucleotide polymorphism at position 331 is presence of C and/or T.

In another embodiment of the invention preferably the method for diagnosis described herein is one in which the single nucleotide polymorphism at position 436 is presence of C and/or T.

In another embodiment of the invention preferably the method for diagnosis described herein is one in which the single nucleotide polymorphism at position 676 is presence of C and/or T.

In another embodiment of the invention preferably the method for diagnosis described herein is one in which the single nucleotide polymorphism at position 1010 is presence of C and/or A.

In another embodiment of the invention preferably the method for diagnosis described herein is one in which the single nucleotide polymorphism at position 1115 is presence of C and/or T.

The method for diagnosis is preferably one in which the sequence is determined by a method selected from amplification refractory mutation system, minisequencing and restriction fragment length polymorphism.

In another aspect of the invention we provide a method for the diagnosis of α_4 integrin subunit ligand-mediated disease, which method comprises:

i) obtaining sample nucleic acid from an individual,

ii) detecting the presence or absence of a variant nucleotide at one or more of positions: positions 740, 2273, 2446, 3311 and 3506 in the coding region of α_4 integrin subunit gene as defined by the positions in EMBL ACCESSION NO. L12002;

position 967 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. L26509; and

positions 184, 238, 331, 436, 676, 1010, or 1115 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. M26841; and

iii) determining the status of the individual by reference to polymorphism in the α_4 integrin subunit gene.

Preferred variations are as follows. Allelic variation at position 740 consists of a single base substitution from C (the published base), preferably to T. Allelic variation at position 2273 consists of a single base substitution from A (the published base), preferably to G. Allelic variation at position 2446 consists of a single base substitution from C (the published base), preferably to T. Allelic variation at position 3311 consists of a single base substitution from T (the published base), preferably to C. Allelic variation at position 3506 consists of a single base substitution from C (the published base), preferably to T. Allelic variation at position 967 consists of a single base substitution from G (the published base), preferably to A. Allelic variation at position 184 consists of a single base substitution from A (the published base), preferably to G. Allelic variation at position 238 consists of a single base substitution from C (the published base), preferably to T. Allelic variation at position 331 consists of a single base substitution from C (the published base), preferably to T. Allelic variation at position 436 consists of a single base substitution from C (the published base), preferably to T. Allelic variation at position 676 consists of a single base substitution from C (the published base), preferably to T. Allelic variation at position 1010 consists of a single base substitution from C (the published base), preferably to A. Allelic variation at position 1115 consists of a single base substitution from C (the published base), preferably to T.

The status of the individual may be determined by reference to allelic variation at any one or more positions optionally in combination with any other polymorphism in the gene that is (or becomes) known.

The test sample of nucleic acid is conveniently a sample of blood, bronchoalveolar lavage fluid, sputum, or other body fluid or tissue obtained from an individual. It will be appreciated that the test sample may equally be a nucleic acid sequence corresponding to the sequence in the test sample, that is to say that all or a part of the region in the sample nucleic acid may firstly be amplified using any convenient technique e.g. PCR, before analysis of allelic variation.

It will be apparent to the person skilled in the art that there are a large number of analytical procedures which may be used to detect the presence or absence of variant

nucleotides at one or more polymorphic positions of the invention. In general, the detection of allelic variation requires a mutation discrimination technique, optionally an amplification reaction and optionally a signal generation system. Table 1 lists a number of mutation detection techniques, some based on the PCR. These may be used in combination with a number of signal generation systems, a selection of which is listed in Table 2. Further amplification techniques are listed in Table 3. Many current methods for the detection of allelic variation are reviewed by Nollau *et al.*, Clin. Chem. **43**, 1114-1120, 1997; and in standard textbooks, for example "Laboratory Protocols for Mutation Detection", Ed. by U. Landegren, Oxford University Press, 1996 and "PCR", 2nd Edition by Newton & Graham, BIOS Scientific Publishers Limited, 1997.

Abbreviations:

ALEX™	Amplification refractory mutation system linear extension
APEX	Arrayed primer extension
ARMS™	Amplification refractory mutation system
b-DNA	Branched DNA
CMC	Chemical mismatch cleavage
bp	base pair
COPS	Competitive oligonucleotide priming system
DGGE	Denaturing gradient gel electrophoresis
FRET	Fluorescence resonance energy transfer
LCR	Ligase chain reaction
MAdCAM-1	mucosal addressin cell adhesion molecule-1
MALDITOF-MS	matrix assisted laser desorption ionisation time of flight mass spectrometry
MASDA	Multiple allele specific diagnostic assay
NASBA	Nucleic acid sequence based amplification
OLA	Oligonucleotide ligation assay
PCR	Polymerase chain reaction
PTT	Protein truncation test
RFLP	Restriction fragment length polymorphism
SDA	Strand displacement amplification

SNP	Single nucleotide polymorphism
SSCP	Single-strand conformation polymorphism analysis
SSR	Self sustained replication
TGGE	Temperature gradient gel electrophoresis
VCAM-1	Vascular Cell Adhesion Molecule-1
VLA-4	Very Late Antigen-4

Table 1 - Mutation Detection Techniques

General: DNA sequencing, Sequencing by hybridisation

Scanning: PTT*, SSCP, DGGE, TGGE, Cleavase, Heteroduplex analysis, CMC, Enzymatic mismatch cleavage

* Note: not useful for detection of promoter polymorphisms.

Hybridisation Based

Solid phase hybridisation: Dot blots, MASDA, Reverse dot blots, Oligonucleotide arrays (DNA Chips)

Solution phase hybridisation: Taqman™ - US-5210015 & US-5487972 (Hoffmann-La Roche), Molecular Beacons - Tyagi *et al* (1996), Nature Biotechnology, **14**, 303; WO 95/13399 (Public Health Inst., New York)

Extension Based: ARMS™, ALEX™ - European Patent No. EP 332435 B1 (Zeneca Limited), COPS - Gibbs *et al* (1989), Nucleic Acids Research, **17**, 2347.

Incorporation Based: Mini-sequencing, APEX

Restriction Enzyme Based: RFLP, Restriction site generating PCR

Ligation Based: OLA

Other: Invader assay

Table 2 - Signal Generation or Detection Systems

Fluorescence: FRET, Fluorescence quenching, Fluorescence polarisation - United Kingdom Patent No. 2228998 (Zeneca Limited)

Other: Chemiluminescence, Electrochemiluminescence, Raman, Radioactivity, Colorimetric, Hybridisation protection assay, Mass spectrometry *e.g.* MALDITOF-MS

Table 3 - Further Amplification Methods

SSR, NASBA, LCR, SDA, b-DNA

Preferred mutation detection techniques include ARMS™, ALEX™, COPS, Taqman, Molecular Beacons, RFLP, and restriction site based PCR and FRET techniques.

Particularly preferred methods include ARMS™ and RFLP based methods. ARMS™ is an especially preferred method.

In a further aspect, the diagnostic methods of the invention are used to assess the efficacy of therapeutic compounds in the treatment of α_4 integrin subunit ligand mediated diseases such as autoimmune, allergic and vascular inflammatory diseases.

Assays, for example reporter-based assays, may be devised to detect whether one or more of the above polymorphisms affect transcription levels and/or message stability.

Individuals who carry particular allelic variants of the α_4 integrin subunit gene may therefore exhibit differences in their ability to regulate protein biosynthesis under different physiological conditions and may display altered abilities to react to different diseases. In addition, differences in protein regulation arising as a result of allelic variation may have a direct effect on the response of an individual to drug therapy. The diagnostic methods of the invention may be useful both to predict the clinical response to such agents and to determine therapeutic dose.

In a further aspect, the diagnostic methods of the invention, are used to assess the predisposition and/or susceptibility of an individual to diseases mediated by α_4 integrin subunit ligands. This may be particularly relevant in the development of autoimmune, allergic and vascular inflammatory diseases and other diseases which are modulated by α_4 integrin subunit interactions. The present invention may be used to recognise individuals who are particularly at risk from developing these conditions.

In a further aspect, the diagnostic methods of the invention are used in the development of new drug therapies which selectively target one or more allelic variants of the α_4 integrin subunit gene. Identification of a link between a particular allelic variant and predisposition to disease development or response to drug therapy may have a significant impact on the design of new drugs. Drugs may be designed to regulate the biological activity of variants implicated in the disease process whilst minimising effects on other variants.

In a further diagnostic aspect of the invention the presence or absence of variant nucleotides is detected by reference to the loss or gain of, optionally engineered, sites recognised by restriction enzymes. In the accompanying Example 2 we provide details of convenient engineered restriction enzyme sites that are lost or gained as a result of a polymorphism of the invention.

According to another aspect of the present invention there is provided a nucleic acid comprising any one of the following polymorphisms:

the nucleic acid of EMBL ACCESSION No. L12002 with T at position 740 as defined by the position in EMBL ACCESSION No. L12002;

the nucleic acid of EMBL ACCESSION No. L12002 with G at position 2273 as defined by the position in EMBL ACCESSION No. L12002;

the nucleic acid of EMBL ACCESSION No. L12002 with T at position 2446 as defined by the position in EMBL ACCESSION No. L12002;

the nucleic acid of EMBL ACCESSION No. L12002 with C at position 3311 as defined by the position in EMBL ACCESSION No. L12002;

the nucleic acid of EMBL ACCESSION No. L12002 with T at position 3506 as defined by the position in EMBL ACCESSION No. L12002;

the nucleic acid of EMBL ACCESSION No. L26059 with A at position 967 as defined by the position in EMBL ACCESSION No. L26059;

the nucleic acid of EMBL ACCESSION No. M26841 with G at position 184 as defined by the position in EMBL ACCESSION No. M26841;

the nucleic acid of EMBL ACCESSION No. M26841 with T at position 238 as defined by the position in EMBL ACCESSION No. M26841;

the nucleic acid of EMBL ACCESSION No. M26841 with T at position 331 as defined by the position in EMBL ACCESSION No. M26841;

the nucleic acid of EMBL ACCESSION No. M26841 with T at position 436 as defined by the position in EMBL ACCESSION No. M26841;

the nucleic acid of EMBL ACCESSION No. M26841 with T at position 676 as defined by the position in EMBL ACCESSION No. M26841;

the nucleic acid of EMBL ACCESSION No. M26841 with A at position 1010 as defined by the position in EMBL ACCESSION No. M26841;

the nucleic acid of EMBL ACCESSION No. M26841 with T at position 1115 as defined by the position in EMBL ACCESSION No. M26841;

or a complementary strand thereof or an antisense sequence for a coding region or a fragment thereof of at least 20 bases comprising at least one polymorphism.

Fragments are at least 17 bases, more preferably at least 20 bases, more preferably at least 30 bases. The nucleic acid of the invention does not encompass naturally occuring nucleic acid as it occurs in nature, for example, the nucleic acid is at least partially purified from at least one component with which it occurs naturally. Preferably the nucleic acid is at least 30% pure, more preferably at least 60% pure, more preferably at least 90% pure, more preferably at least 95% pure, and more preferably at least 99% pure.

Novel sequence disclosed herein, may be used in another embodiment of the invention to regulate expression of the gene in cells by the use of antisense constructs. To enable methods of down-regulating expression of the gene of the present invention in mammalian cells, an example antisense expression construct can be readily constructed for instance using the pREP10 vector (Invitrogen Corporation). Transcripts are expected to inhibit translation of the gene in cells transfected with this type construct. Antisense transcripts are effective for inhibiting translation of the native gene transcript, and capable of inducing the effects (e.g., regulation of tissue physiology) herein described. Oligonucleotides which are complementary to and hybridizable with any portion of novel gene mRNA disclosed herein are contemplated for therapeutic use. U.S. Patent No. 5,639,595, Identification of Novel Drugs and Reagents, issued Jun. 17, 1997, wherein methods of identifying oligonucleotide sequences that display in vivo activity are thoroughly described, is herein incorporated by reference. Expression vectors containing random oligonucleotide sequences derived from previously known polynucleotides are transformed into cells. The cells are then assayed for a phenotype resulting from the desired activity of the oligonucleotide. Once cells with the desired phenotype have been identified, the sequence of the oligonucleotide having the desired activity can be identified. Identification may be accomplished by recovering the vector or by polymerase chain reaction (PCR) amplification and sequencing the region containing the inserted nucleic acid material.nucleotide molecules can be synthesized for antisense therapy. These antisense molecules may be DNA, stable derivatives of DNA such as phosphorothioates or methylphosphonates, RNA, stable derivatives of RNA such as 2'-O-alkylRNA, or other oligonucleotide mimetics. U.S. Patent No. 5,652,355, Hybrid Oligonucleotide

Phosphorothioates, issued July 29, 1997, and U.S. Patent No. 5,652,356, Inverted Chimeric and Hybrid Oligonucleotides, issued July 29, 1997, which describe the synthesis and effect of physiologically-stable antisense molecules, are incorporated by reference. Antisense molecules may be introduced into cells by microinjection, liposome encapsulation or by expression from vectors harboring the antisense sequence.

According to another aspect of the invention there is provided use of a nucleic acid sequence comprising at least one of the polymorphisms in the promoter disclosed herein to identify compounds that modify expression of the human α_4 integrin subunit gene. Modification of expression includes inhibition or enhancement of expression. This is conveniently done by measuring expression levels of a reporter gene (for example beta-galactosidase) under the control of the promoter in transfected host cells in the presence or absence of test compounds. Suitable test compounds include polynucleotides capable of binding to the promoter through triplex strand formation. Accordingly, suitable compounds can be identified for therapeutic use which alter native gene expression either up or down as appropriate for the relevant disease to be treated. The reader is directed to the following references on nucleic acid triplex formation and uses: Progress in developments of Triplex-Based strategies: Giovannangeli C; Helene C: Antisense and Nucleic Acid Drug Development / 7/4 (413-421) /1997; Recent developments in triple-helix regulation of gene expression: Neidle S: Anti-Cancer Drug Design / 12/5 (433-442) /1997; Triplex DNA: Fundamentals, advances, and potential applications for gene therapy: Chan PP; Glazer PM : Journal of Molecular Medicine / 75/4 (267-282) /1997; Oligonucleotide directed triple helix formation: Sun J-S; Garestier T; Helene C: Current Opinion in Structural Biology / 6/3 (327-333) /1996; C Mayfield, M Squibb, D Miller (1994) Inhibition of nuclear protein binding to the human Ki-ras promoter by triplex-forming oligonucleotides Biochemistry 33,3358-3363; WM Olivas, LJ Maher (1996) Binding of DNA oligonucleotides to sequences in the promoter of the human bcl-2 gene Nucleic Acids Research 24, 1758-1764; C Mayfield, S Ebinghaus, J Gees, D Jones, B Rodu, M Squibb, D Miller (1994) Triplex formation by the human HA-ras promoter inhibits Sp1 binding and in vitro transcription J Biol Chem 269,18232-18238; and JE Gee, GR Revankar, TS Rao, ME Hogan (1995) Triplex formation at the rat neu gene utilizing imidazole and 2'-deoxy-6-thioguanosine base substitutions Biochemistry 34,2042-2048.

According to another aspect of the present invention there is provided a computer readable medium comprising at least one novel polynucleotide sequence of the invention

stored on the medium. The computer readable medium may be used, for example, in homology searching, mapping, haplotyping, genotyping or pharmacogenetic analysis or any other bioinformatic analysis. The reader is referred to Bioinformatics, A practical guide to the analysis of genes and proteins, Edited by A D Baxevanis & B F F Ouellette, John Wiley & Sons, 1988. Any computer readable medium may be used, for example, compact disk, tape, floppy disk, hard drive or computer chips.

The polynucleotide sequences of the invention, or parts thereof, particularly those relating to and identifying the single nucleotide polymorphisms identified herein represent a valuable information source, for example, to characterise individuals in terms of haplotype and other sub-groupings, such as investigation of susceptibility to treatment with particular drugs. These approaches are most easily facilitated by storing the sequence information in a computer readable medium and then using the information in standard bioinformatics programs or to search sequence databases using state of the art searching tools such as "GCC". Thus, the polynucleotide sequences of the invention are particularly useful as components in databases useful for sequence identity and other search analyses. As used herein, storage of the sequence information in a computer readable medium and use in sequence databases in relation to 'polynucleotide or polynucleotide sequence of the invention' covers any detectable chemical or physical characteristic of a polynucleotide of the invention that may be reduced to, converted into or stored in a tangible medium, such as a computer disk, preferably in a computer readable form. For example, chromatographic scan data or peak data, photographic scan or peak data, mass spectrographic data, sequence gel (or other) data.

The invention provides a computer readable medium having stored thereon one or a more polynucleotide sequences of the invention. For example, a computer readable medium is provided comprising and having stored thereon a member selected from the group consisting of: a polynucleotide comprising the sequence of a polynucleotide of the invention, a polynucleotide consisting of a polynucleotide of the invention, a polynucleotide which comprises part of a polynucleotide of the invention, which part includes at least one of the polymorphisms of the invention, a set of polynucleotide sequences wherein the set includes at least one polynucleotide sequence of the invention, a data set comprising or consisting of a polynucleotide sequence of the invention or a part thereof comprising at least one of the polymorphisms identified herein. A computer based method is also provided for performing sequence identification, said method comprising the steps of providing a polynucleotide

sequence comprising a polymorphism of the invention in a computer readable medium; and comparing said polymorphism containing polynucleotide sequence to at least one other polynucleotide or polypeptide sequence to identify identity (homology), i.e. screen for the presence of a polymorphism.

The invention further provides nucleotide primers which can detect the polymorphisms of the invention.

According to another aspect of the present invention there is provided an allele specific primer capable of detecting a α_4 integrin subunit gene polymorphism at one or more of positions:

positions 740, 2273, 2446, 3311 and 3506 in the coding region of α_4 integrin subunit gene as defined by the positions in EMBL ACCESSION NO. L12002;

position 967 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. L26509; and

positions 184, 238, 331, 436, 676, 1010, or 1115 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. M26841;

An allele specific primer is used, generally together with a constant primer, in an amplification reaction such as a PCR reaction, which provides the discrimination between alleles through selective amplification of one allele at a particular sequence position e.g. as used for ARMS™ assays. The allele specific primer is preferably 17- 50 nucleotides, more preferably about 17-35 nucleotides, more preferably about 17-30 nucleotides.

An allele specific primer preferably corresponds exactly with the allele to be detected but derivatives thereof are also contemplated wherein about 6-8 of the nucleotides at the 3' terminus correspond with the allele to be detected and wherein up to 10, such as up to 8, 6, 4, 2, or 1 of the remaining nucleotides may be varied without significantly affecting the properties of the primer.

Primers may be manufactured using any convenient method of synthesis. Examples of such methods may be found in standard textbooks, for example "Protocols for Oligonucleotides and Analogues; Synthesis and Properties," Methods in Molecular Biology Series; Volume 20; Ed. Sudhir Agrawal, Humana ISBN: 0-89603-247-7; 1993; 1st Edition. If required the primer(s) may be labelled to facilitate detection.

According to another aspect of the present invention there is provided an allele-specific oligonucleotide probe capable of detecting a α_4 integrin subunit gene polymorphism at one or more of positions:

positions 740, 2273, 2446, 3311 and 3506 in the coding region of α_4 integrin subunit gene as defined by the positions in EMBL ACCESSION NO. L12002;

position 967 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. L26509; and

positions 184, 238, 331, 436, 676, 1010, or 1115 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. M26841;

The allele-specific oligonucleotide probe is preferably 17- 50 nucleotides, more preferably about 17-35 nucleotides, more preferably about 17-30 nucleotides.

The design of such probes will be apparent to the molecular biologist of ordinary skill. Such probes are of any convenient length such as up to 50 bases, up to 40 bases, more conveniently up to 30 bases in length, such as for example 8-25 or 8-15 bases in length. In general such probes will comprise base sequences entirely complementary to the corresponding wild type or variant locus in the gene. However, if required one or more mismatches may be introduced, provided that the discriminatory power of the oligonucleotide probe is not unduly affected. The probes of the invention may carry one or more labels to facilitate detection.

According to another aspect of the present invention there is provided a diagnostic kit comprising an allele specific oligonucleotide probe of the invention and/or an allele-specific primer of the invention.

The diagnostic kits may comprise appropriate packaging and instructions for use in the methods of the invention. Such kits may further comprise appropriate buffer(s) and polymerase(s) such as thermostable polymerases, for example taq polymerase.

In another aspect of the invention, the single nucleotide polymorphisms of this invention may be used as genetic markers in linkage studies. This particularly applies to the polymorphisms at 2273 and/or 3311 and/ or 1010 because of their relatively high frequency (see below). The α_4 integrin subunit gene has been mapped to chromosome 2q31-q32 (Fernandez-Ruiz *et al*, Europ. J. Immunol. **22**: 587-590, 1992).

Low frequency polymorphisms may be particularly useful for haplotyping as described below. A haplotype is a set of alleles found at linked polymorphic sites (such as within a gene) on a single (paternal or maternal) chromosome. If recombination within the gene is random,

there may be as many as 2^n haplotypes, where 2 is the number of alleles at each SNP and n is the number of SNPs. One approach to identifying mutations or polymorphisms which are correlated with clinical response is to carry out an association study using all the haplotypes that can be identified in the population of interest. The frequency of each haplotype is limited by the frequency of its rarest allele, so that SNPs with low frequency alleles are particularly useful as markers of low frequency haplotypes. As particular mutations or polymorphisms associated with certain clinical features, such as adverse or abnormal events, are likely to be of low frequency within the population, low frequency SNPs may be particularly useful in identifying these mutations (for examples see: Linkage disequilibrium at the cystathionine beta synthase (CBS) locus and the association between genetic variation at the CBS locus and plasma levels of homocysteine. *Ann Hum Genet* (1998) **62**:481-90, De Stefano V, Dekou V, Nicaud V, Chasse JF, London J, Stansbie D, Humphries SE, and Gudnason V; and Variation at the von willebrand factor (vWF) gene locus is associated with plasma vWF:Ag levels: identification of three novel single nucleotide polymorphisms in the vWF gene promoter. *Blood* (1999) **93**:4277-83, Keightley AM, Lam YM, Brady JN, Cameron CL, Lillicrap D).

According to another aspect of the present invention there is provided an allelic variant of the human integrin α_4 polypeptide having a methionine at position 679 or a fragment thereof comprising at least 10 amino acids provided that the fragment comprises the allelic variant at position 679.

Fragments of integrin α_4 polypeptide are at least 10 amino acids, more preferably at least 15 amino acids, more preferably at least 20 amino acids. The polypeptide of the invention does not encompass naturally occuring polypeptide as it occurs in nature, for example, the polypeptide is at least partially purified from at least one component with which it occurs naturally. Preferably the polypeptide is at least 30% pure, more preferably at least 60% pure, more preferably at least 90% pure, more preferably at least 95% pure, and more preferably at least 99% pure.

According to another aspect of the present invention there is provided an antibody specific for an allelic variant of human integrin α_4 polypeptide having a methionine at position 679 or a fragment thereof comprising at least 10 amino acids provided that the fragment comprises the allelic variant at position 679

Antibodies can be prepared using any suitable method. For example, purified polypeptide may be utilized to prepare specific antibodies. The term "antibodies" is meant to

include polyclonal antibodies, monoclonal antibodies, and the various types of antibody constructs such as for example $F(ab')_2$, Fab and single chain Fv. Antibodies are defined to be specifically binding if they bind the T679M variant of integrin α_4 with a K_a of greater than or equal to about 10^7 M^{-1}. Affinity of binding can be determined using conventional techniques, for example those described by Scatchard et al., *Ann. N.Y. Acad. Sci.*, 51:660 (1949).

Polyclonal antibodies can be readily generated from a variety of sources, for example, horses, cows, goats, sheep, dogs, chickens, rabbits, mice or rats, using procedures that are well-known in the art. In general, antigen is administered to the host animal typically through parenteral injection. The immunogenicity of antigen may be enhanced through the use of an adjuvant, for example, Freund's complete or incomplete adjuvant. Following booster immunizations, small samples of serum are collected and tested for reactivity to antigen. Examples of various assays useful for such determination include those described in: *Antibodies: A Laboratory Manual*, Harlow and Lane (eds.), Cold Spring Harbor Laboratory Press, 1988; as well as procedures such as countercurrent immuno-electrophoresis (CIEP), radioimmunoassay, radioimmunoprecipitation, enzyme-linked immuno-sorbent assays (ELISA), dot blot assays, and sandwich assays, see U.S. Patent Nos. 4,376,110 and 4,486,530.

Monoclonal antibodies may be readily prepared using well-known procedures, see for example, the procedures described in U.S. Patent Nos. RE 32,011, 4,902,614, 4,543,439 and 4,411,993; Monoclonal Antibodies, Hybridomas: *A New Dimension in Biological Analyses*, Plenum Press, Kennett, McKearn, and Bechtol (eds.), (1980).

The monoclonal antibodies of the invention can be produced using alternative techniques, such as those described by Alting-Mees et al., "Monoclonal Antibody Expression Libraries: A Rapid Alternative to Hybridomas", *Strategies in Molecular Biology* 3: 1-9 (1990) which is incorporated herein by reference. Similarly, binding partners can be constructed using recombinant DNA techniques to incorporate the variable regions of a gene that encodes a specific binding antibody. Such a technique is described in Larrick et al., *Biotechnology*, 7: 394 (1989).

Once isolated and purified, the antibodies may be used to detect the presence of antigen in a sample using established assay protocols.

According to another aspect of the present invention there is provided a method of treating a human in need of treatment with a α_4 integrin subunit ligand antagonist drug in which the method comprises:

i) diagnosis of a single nucleotide polymorphism in α_4 integrin subunit gene in the human, which diagnosis comprises determining the sequence of the nucleic acid at one or more of positions:

positions 740, 2273, 2446, 3311 and 3506 in the coding region of α_4 integrin subunit gene as defined by the positions in EMBL ACCESSION NO. L12002;

position 967 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. L26509; and

positions 184, 238, 331, 436, 676, 1010, or 1115 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. M26841;

and determining the status of the human by reference to polymorphism in the α_4 integrin subunit gene; and

ii) administering an effective amount of a α_4 integrin subunit ligand antagonist .

Preferably determination of the status of the human is clinically useful. Examples of clinical usefulness include deciding which antagonist drug or drugs to administer and/or in deciding on the effective amount of the drug or drugs.

α_4 integrin subunit ligand antagonist drugs have been disclosed in the following publications: international patent application WO 97/49731, Zeneca Limited; international patent application WO 97/02289, Zeneca Limited; international patent application WO 96/20216, Zeneca Limited; US patent 5510332, Texas Biotechnology; international patent application WO 96/01644, Athena Neurosciences; international patent application WO 96/01644, Athena Neurosciences and; international patent application WO 96/00581, Zeneca Limited. A α_4 integrin subunit ligand antagonist drug may act directly at α_4 integrin subunit heterodimer and/or at a ligand, such as VCAM, CS-1 fibronectin or MAdCAM-1 which binds to α_4 integrin subunit heterodimers, $\alpha_4\beta_1$ or $\alpha_4\beta_7$. VLA-4 antagonists as anti-inflammatory agents have been reviewed by Lin KC & Castro AC in Curr. Opin. Chem. Biol. (1998), 2: 453-457.

According to another aspect of the present invention there is provided use of a α_4 integrin subunit ligand antagonist drug in preparation of a medicament for treating a α_4 integrin subunit ligand mediated disease in a human diagnosed as having a single nucleotide polymorphism at one or more of positions:

positions 740, 2273, 2446, 3311 and 3506 in the coding region of α_4 integrin subunit gene as defined by the positions in EMBL ACCESSION NO. L12002;

position 967 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. L26509; and

positions 184, 238, 331, 436, 676, 1010, or 1115 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. M26841.

According to another aspect of the present invention there is provided a pharmaceutical pack comprising α_4 integrin subunit ligand antagonist drug and instructions for administration of the drug to humans diagnostically tested for a single nucleotide polymorphism at one or more of positions:

positions 740, 2273, 2446, 3311 and 3506 in the coding region of α_4 integrin subunit gene as defined by the positions in EMBL ACCESSION NO. L12002;

position 967 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. L26509; and

positions 184, 238, 331, 436, 676, 1010, or 1115 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. M26841.

The invention will now be illustrated but not limited by reference to the following Examples. All temperatures are in degrees Celsius.

In the Examples below, unless otherwise stated, the following methodology and materials have been applied.

AMPLITAQ™ ,available from Perkin-Elmer Cetus, is used as the source of thermostable DNA polymerase.

General molecular biology procedures can be followed from any of the methods described in "Molecular Cloning - A Laboratory Manual" Second Edition, Sambrook, Fritsch and Maniatis (Cold Spring Harbor Laboratory, 1989).

Electropherograms were obtained in a standard manner: data was collected by ABI377 data collection software and the wave form generated by ABI Prism sequencing analysis (2.1.2).

Example 1

Identification of Polymorphisms

1. Methods

c-DNA Preparation

RNA was prepared from lymphoblastoid cell lines from Caucasian donors using standard laboratory protocols (Chomczynski and Sacchi, Anal. Biochem. **162**, 156-159, 1987) and used to generate first strand cDNA (Gubler and Hoffman, Gene **25**, 263-269, 1983).

Genomic DNA Preparation

DNA was prepared from frozen blood samples collected in EDTA following protocol I (Molecular Cloning: A Laboratory Manual, p392, Sambrook, Fritsch and Maniatis, 2nd Edition, Cold Spring Harbor Press, 1989) with the following modifications. The thawed blood was diluted in an equal volume of standard saline citrate instead of phosphate buffered saline to remove lysed red blood cells. Samples were extracted with phenol, then phenol/chloroform and then chloroform rather than with three phenol extractions. The DNA was dissolved in deionised water.

Template Preparation

Templates were prepared by PCR using the oligonucleotide primers and annealing temperatures set out below. The extension temperature was 72° and denaturation temperature 94°; each step was 1 minute. Generally 100 pg cDNA or 50ng genomic DNA was used in each reaction and subjected to 40 cycles of PCR.

cDNA Fragment	Forward Oligo	Reverse Oligo	Annealing Temp	$MgCl_2$	DMSO
290-811	290-310	790-811	64°	1.0 mM	5 %
2119-2630	2119-2139	2609-2630	64°	1.5 mM	0
2961-3550	2961-2982	3528-3550	60°	1.0 mM	0

For dye-primer sequencing the forward primers were modified to include M13 forward sequence (ABI protocol P/N 402114, Applied Biosystems) at the 5' end of the oligonucleotides.

Dye Primer Sequencing

Dye-primer sequencing using M13 forward and reverse primers was as described in the ABI protocol P/N 402114 for the ABI Prism™ dye primer cycle sequencing core kit with "AmpliTaq FS"™ DNA polymerase, modified in that the annealing temperature was 45° and DMSO was added to the cycle sequencing mix to a final concentration of 5 %.

The extension reactions for each base were pooled, ethanol/sodium acetate precipitated, washed and resuspended in formamide loading buffer.

4.25 % Acrylamide gels were run on an automated sequencer (ABI 377, Applied Biosystems).

2. Results

Novel Polymorphisms

Integrin Alpha-4 cDNA

EMBL Accession No L12002

ID HSITGA4

Ref Takada *et al*, EMBO J. **8**: 1361-1368, 1989

Position	Published	Variant	Amino acid change	RFLP	Frequency
740	C	T		NO	1/52
2273	A	G		eng'+Acl I	32/54
2446	C	T	Thr-Met (T679M)	eng'+Bsp HI	1/54
3311	T	C		eng'-Sph I	29/54
3506	C	T		eng'+Spe I	2/52

Frequency is the allele frequency of the variant allele in European control subjects .

"eng" = engineered RFLP

Example 2

Engineered restriction site for detection of polymorphisms

Standard methodology can be used to detect the polymorphism at positions 2273, 2446, 3311 and 3506 (as defined by the position in EMBL ACCESSION NO. L12002) based on the materials set out below using a cDNA template.

Position	**Diagnostic Fragment**	**Forward primer**	**Reverse primer**
2273	2119-2297	2119-2139	2274-2297 Acl I

2446	2422-2630	2422-2445 Bsp HI	2609-2630
3311	2961-3335	2961-2982	3312-3335 Sph I
3506	3481-3564	3481-3505 Spe I	3542-3564

Primer Sequences 5′-3′

2274-2297 Acl I GGCACAAAACCTTGCAAAGTTTAA (SEQ ID NO:1)
2422-2445 Bsp HI ATGCTGGAGATGATGCATATGTCA (SEQ ID NO:2)
3312-3335 Sph I ATGATGTAGTCCTTCCAGTAGAGC (SEQ ID NO:3)
3481-3505 Spe I GAAGAGACAGTTGGAGTTATATCAC (SEQ ID NO:4)

G at position 2273 creates an Acl I site in the diagnostic fragment, 2119-2297, described above. T at position 2446 creates a Bsp HI site in the diagnostic fragment, 2422-2630, described above. T at position 3311 creates a Sph I site in the diagnostic fragment, 2961-3335, described above. T at position 3506 creates a Spe I site in the diagnostic fragment, 3481-3564, described above.

Example 3

Integrin alpha-4 promoter polymorphisms

The sequences scanned are covered by two EMBL entries, Accession nos L26059 and M62841. The polymorphisms set out below were identified.

Position	Published	Variant	RFLP	Frequency
967 of L26059	G	A	+ eng Msc I	1/54
184 of M62841	A	G	- Tsp 509 I	1/64
238 of M62841	C	T	+ eng Dra I	2/62
331 of M62841	C	T	- Sma I	3/62
436 of M62841	C	T		1/66
676 of M62841	C	T	- Bfa I	1/66
1010 of M62841	C	A		10/60
1115 of M62841	C	T	+ eng Eco RI	1/60

Frequency is the allele frequency of the variant allele in control subjects.

The following alterations in transcription factor binding sites associated with the polymorphisms are noted.

Position of M62841	Gain of TF site	Loss of TF site
184	HNF-1-HP1 rev	
238	PEA CS-rev, HC1 rev, PEA3-RS rev, kappa4	
436	AP2 CS4, Pu box rev	Histone H4 CS2 rev
1115		Apa A

Example 4

Detection of Promoter Polymorphisms using Engineered RFLPs

Engineered RFLPs were used to detect three of the promoter polymorphisms in a PCR assay as set out below.

Position	Diagnostic Fragment	Forward Primer	Reverse Primer
L26059, 967	944-1202	944-966 Msc I	1181-1202
M62841, 238	3-262	3-32	239-262 Dra I
M62841, 1115	1094-1267	1094-1114 Eco RI	1248-1267

Primers

944-966 Msc I ACTTCTGAAACCCAGAGCTGGCC(SEQ ID NO:5)

239-262 Dra I ACCCCAACAGAGAGGTTGGTTTAA(SEQ ID NO:6)

1094-1114 Eco RI CCCGTTGGCCAACCGTCGAAT(SEQ ID NO:7)

A at position 967 (L26059) creates a Msc I site in the fragment 944-1202 using the primers described above.

T at position 238 (M62841) creates a Dra I site in the fragment 3-262 using the primers described above.

T at position 1115(M62841) creates an Eco RI site in the fragment 1094-1267 using the primers described above.

Example 5

Detection of Polymorphism using Minisequencing

Minisequencing was used to detect the promoter polymorphism at position 1010 of M62841 1010 as set out below.

Oligonucleotide, GAAGAGGAGGGGAAGTCG (SEQ ID NO:8), was used as a primer in a minisequencing reaction. The C-A polymorphism is detected by the incorporation of ddGTP or ddTTP which can be resolved, for example, by MALDITOF-MS.

Sequence Listing Free Text

<223> Description of Artificial Sequence:PCR primer

CLAIMS

1 A method for the diagnosis of a single nucleotide polymorphism in a α_4 integrin subunit in a human, which method comprises determining the sequence of nucleic acid of the human at one or more of the following positions:

positions 740, 2273, 2446, 3311 and 3506 in the coding region of α_4 integrin subunit gene as defined by the positions in EMBL ACCESSION NO. L12002;

position 967 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. L26509; and

positions 184, 238, 331, 436, 676, 1010, or 1115 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. M26841;

and determining the status of the human by reference to polymorphism in the α_4 integrin subunit gene.

2 A method for diagnosis according to claim 1 in which the single nucleotide polymorphisms are further defined as:

the single nucleotide polymorphism at position 740 is presence of C and/or T;

the single nucleotide polymorphism at position 2273 is presence of A and/or G;

the single nucleotide polymorphism at position 2446 is presence of C and/or T;

the single nucleotide polymorphism at position 3311 is presence of T and/or C;

the single nucleotide polymorphism at position 3506 is presence of C and/or T;

the single nucleotide polymorphism at position 967 is presence of G and/or A;

the single nucleotide polymorphism at position 184 is presence of A and/or G;

the single nucleotide polymorphism at position 238 is presence of C and/or T;

the single nucleotide polymorphism at position 331 is presence of C and/or T;

the single nucleotide polymorphism at position 436 is presence of C and/or T;

the single nucleotide polymorphism at position 676 is presence of C and/or T;

the single nucleotide polymorphism at position 1010 is presence of C and/or A; and

the single nucleotide polymorphism at position 1115 is presence of C and/or T.

3 A method for diagnosis according to claim 1 in which the method comprises determining the sequence of nucleic acid of the human at position 2446 for presence of C and/or T.

4 A method for diagnosis according to any preceding claim in which the sequence is determined by a method selected from amplification refractory mutation system, minisequencing and restriction fragment length polymorphism.

5 A nucleic acid comprising any one of the following polymorphisms:

the nucleic acid of EMBL ACCESSION No. L12002 with T at position 740 as defined by the position in EMBL ACCESSION No. L12002;

the nucleic acid of EMBL ACCESSION No. L12002 with G at position 2273 as defined by the position in EMBL ACCESSION No. L12002;

the nucleic acid of EMBL ACCESSION No. L12002 with T at position 2446 as defined by the position in EMBL ACCESSION No. L12002;

the nucleic acid of EMBL ACCESSION No. L12002 with C at position 3311 as defined by the position in EMBL ACCESSION No. L12002;

the nucleic acid of EMBL ACCESSION No. L12002 with T at position 3506 as defined by the position in EMBL ACCESSION No. L12002;

the nucleic acid of EMBL ACCESSION No. L26059 with A at position 967 as defined by the position in EMBL ACCESSION No. L26059;

the nucleic acid of EMBL ACCESSION No. M26841 with G at position 184 as defined by the position in EMBL ACCESSION No. M26841;

the nucleic acid of EMBL ACCESSION No. M26841 with T at position 238 as defined by the position in EMBL ACCESSION No. M26841;

the nucleic acid of EMBL ACCESSION No. M26841 with T at position 331 as defined by the position in EMBL ACCESSION No. M26841;

the nucleic acid of EMBL ACCESSION No. M26841 with T at position 436 as defined by the position in EMBL ACCESSION No. M26841;

the nucleic acid of EMBL ACCESSION No. M26841 with T at position 676 as defined by the position in EMBL ACCESSION No. M26841;

the nucleic acid of EMBL ACCESSION No. M26841 with A at position 1010 as defined by the position in EMBL ACCESSION No. M26841;

the nucleic acid of EMBL ACCESSION No. M26841 with T at position 1115 as defined by the position in EMBL ACCESSION No. M26841;

or a complementary strand thereof or an antisense sequence for a coding region or a fragment thereof of at least 20 bases comprising at least one polymorphism.

6 A computer readable medium comprising at least one nucleic acid sequence as defined in claim 5 stored on the medium.

7 An allele specific primer capable of detecting a α_4 integrin subunit gene polymorphism at one or more of positions:

positions 740, 2273, 2446, 3311 and 3506 in the coding region of α_4 integrin subunit gene as defined by the positions in EMBL ACCESSION NO. L12002;

position 967 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. L26509; and

positions 184, 238, 331, 436, 676, 1010, or 1115 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. M26841.

8 An allele-specific oligonucleotide probe capable of detecting a α_4 integrin subunit gene polymorphism at one or more of positions:

positions 740, 2273, 2446, 3311 and 3506 in the coding region of α_4 integrin subunit gene as defined by the positions in EMBL ACCESSION NO. L12002;

position 967 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. L26509; and

positions 184, 238, 331, 436, 676, 1010, or 1115 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. M26841.

9 An allelic variant of the human integrin α_4 polypeptide having a methionine at position 679 or a fragment thereof comprising at least 10 amino acids provided that the fragment comprises the allelic variant at position 679.

10 Use of a α_4 integrin subunit ligand antagonist drug in preparation of a medicament for treating a α_4 integrin subunit ligand mediated disease in a human diagnosed as having a single nucleotide polymorphism at one or more of positions:

positions 740, 2273, 2446, 3311 and 3506 in the coding region of α_4 integrin subunit gene as defined by the positions in EMBL ACCESSION NO. L12002;

position 967 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. L26509; and

positions 184, 238, 331, 436, 676, 1010, or 1115 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. M26841.

11 Use of a nucleic acid sequence comprising at least one of the following polymorphisms in the promoter:

position 967 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. L26509; and

positions 184, 238, 331, 436, 676, 1010, or 1115 in the promoter region of α_4 integrin subunit gene as defined by the position in EMBL ACCESSION NO. M26841;

to identify compounds that modify expression of the human α_4 integrin subunit gene.

FOR UTILITY/DESIGN CIP/PCT NATIONAL/PLANT ORIGINAL/SUBSTITUTE/SUPPLEMENTAL DECLARATIONS

RULE 63 (37 C.F.R. 1.63) DECLARATION AND POWER OF ATTORNEY FOR PATENT APPLICATION IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

PW FORM Z70390/UST

As a below named inventor, I hereby declare that my residence, post office address and citizenship are as stated below next to my name, and I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the **INVENTION ENTITLED** POLYMORPHISMS IN THE HUMAN ALPHA4 INTEGRIN SUBUNIT GENE, SUITABLE FOR DIAGNOSIS AND TREATMENT OF INTEGRIN LIGAND MEDIATED DISEASES

the specification of which (CHECK applicable BOX(ES))

X A. ☐ is attached hereto.

BOX(ES) → B. ☐ was filed on _____ as U.S. Application No. _____/_____

→ → C. ☒ was filed as PCT International Application No. PCT/ GB99 /03071 on 15.09.1999

and (if applicable to U.S. or PCT application) was amended on _____

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above. I acknowledge the duty to disclose all information known to me to be material to patentability as defined in 37 C.F.R. 1.56. Except as noted below, I hereby claim foreign priority benefits under 35 U.S.C. 119(a)-(d) or 365(b) of any foreign application(s) for patent or inventor's certificate, or 365(a) of any PCT International Application which designated at least one other country than the United States, listed below and have also identified below any foreign application for patent or inventor's certificate, or PCT International Application, filed by me or my assignee disclosing the subject matter claimed in this application and having a filing date (1) before that of the application on which priority is claimed, or (2) if no priority claimed, before the filing date of this application:

PRIOR FOREIGN APPLICATION(S) Number	Country	Day/MONTH/Year Filed	Date first Laid-open or Published	Date Patented or Granted	Priority NOT Claimed
9820339.1	GB	19.09.1998			
9824506.1	GB	10.11.1998			

If more prior foreign applications, X box *at bottom* and continue on attached page.

Except as noted below, I hereby claim domestic priority benefit under 35 U.S.C. 119(e) or 120 and/or 365(c) of the indicated United States applications listed below and PCT international applications listed above or below and, if this is a continuation-in-part (CIP) application, insofar as the subject matter disclosed and claimed in this application is in addition to that disclosed in such prior applications, I acknowledge the duty to disclose all information known to me to be material to patentability as defined in 37 C.F.R. 1.56 which became available between the filing date of each such prior application and the national or PCT international filing date of this application:

PRIOR U.S. PROVISIONAL, NONPROVISIONAL AND/OR PCT APPLICATION(S) Application No. (series code/serial no.)	Day/MONTH/Year Filed	Status pending, abandoned, patented	Priority NOT Claimed

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

And I hereby appoint Pillsbury Winthrop LLP, Intellectual Property Group, telephone number (202) 861-3000 (to whom all communications are to be directed), and persons of that firm who are associated with USPTO Customer No. 909 (see below label) individually and collectively my attorneys to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith and with the resulting patent, and I hereby authorize them to delete from that Customer No. names of persons no longer with their firm, to add new persons of their Firm to that Customer No., and to act and rely on instructions from and communicate directly with the person/assignee/attorney/firm/ organization who/which first sends/sent this case to them and by whom/which I hereby declare that I have consented after full disclosure to be represented unless/until I instruct the above Firm and/or an attorney of that Firm in writing to the contrary.

00909

(1) **INVENTOR'S SIGNATURE:** John E.N. Morten **Date:** 8th February 2001

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Name			
	First	Middle Initial	Family Name
Residence			
	City	State/Foreign Country	Country of Citizenship
Mailing Address			
(include Zip Code)			

☐ FOR ADDITIONAL INVENTORS see attached page.

☐ See additional foreign priorities on attached page (incorporated herein by reference).

Atty. Dkt. No. P_____

(M#)

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